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SEQUENCE LISTING

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<120> METHODS FOR PRESERVING AND/OR STORING CELLS HAVING A NITRILASE
OR NITRILE HYDRATASE ACTIVITY

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<150> PCT/EP2003/014880
<151> 2003-12-24

<150> DE 103 00 500.5
<151> 2003-01-08

<160> 2

<170> PatentIn version 3.3

<210> 1
<211> 1071
<212> DNA
<213> Alcaligenes faecalis

<220>
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<222> (1)...(1068)
<223> coding for nitrilase

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ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct	96		
Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala			
20 25 30			
cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc	144		
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr			
35 40 45			
tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg	192		
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp			
50 55 60			
tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac	240		
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp			
65 70 75 80			
agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att	288		
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile			
85 90 95			
ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg	336		
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu			
100 105 110			
ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc	384		
Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg			
115 120 125			
aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat	432		

Lys	Leu	Lys	Pro	Thr	His	Val	Glu	Arg	Thr	Val	Phe	Gly	Glu	Gly	Tyr	
130						135					140					
gcc	cgt	gat	ctg	att	gtg	tcc	gac	aca	gaa	ctg	gga	cgc	gtc	ggt	gct	480
Ala	Arg	Asp	Leu	Ile	Val	Ser	Asp	Thr	Glu	Leu	Gly	Arg	Val	Gly	Ala	
145						150				155					160	
cta	tgc	tgc	tgg	gag	cat	ttg	tcg	ccc	ttg	agc	aag	tac	gcg	ctg	tac	528
Leu	Cys	Cys	Trp	Glu	His	Leu	Ser	Pro	Leu	Ser	Lys	Tyr	Ala	Leu	Tyr	
						165				170				175		
tcc	cag	cat	gaa	gcc	att	cac	att	gct	gcc	tgg	ccg	tcg	ttt	tcg	cta	576
Ser	Gln	His	Glu	Ala	Ile	His	Ile	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	
						180				185				190		
tac	agc	gaa	cag	gcc	cac	gcc	ctc	agt	gcc	aag	gtg	aac	atg	gct	gcc	624
Tyr	Ser	Glu	Gln	Ala	His	Ala	Leu	Ser	Ala	Lys	Val	Asn	Met	Ala	Ala	
						195				200				205		
tcg	caa	atc	tat	tcg	gtt	gaa	ggc	cag	tgc	ttt	acc	atc	gcc	gcc	agc	672
Ser	Gln	Ile	Tyr	Ser	Val	Glu	Gly	Gln	Cys	Phe	Thr	Ile	Ala	Ala	Ser	
						210				215				220		
agt	gtg	gtc	acc	caa	gag	acg	cta	gac	atg	ctg	gaa	gtg	ggt	gaa	cac	720
Ser	Val	Val	Thr	Gln	Glu	Thr	Leu	Asp	Met	Leu	Glu	Val	Gly	Glu	His	
						225				230				235		240
aac	gcc	ccc	ttg	ctg	aaa	gtg	ggc	ggc	ggc	agt	tcc	atg	att	ttt	gcg	768
Asn	Ala	Pro	Leu	Leu	Lys	Val	Gly	Gly	Gly	Ser	Ser	Met	Ile	Phe	Ala	
						245				250				255		
ccg	gac	gga	cgc	aca	ctg	gct	ccc	tac	ctg	cct	cac	gat	gcc	gag	ggc	816
Pro	Asp	Gly	Arg	Thr	Leu	Ala	Pro	Tyr	Leu	Pro	His	Asp	Ala	Glu	Gly	
						260				265				270		
ttg	atc	att	gcc	gat	ctg	aat	atg	gag	gag	att	gcc	ttc	gcc	aaa	gcg	864
Leu	Ile	Ile	Ala	Asp	Leu	Asn	Met	Glu	Glu	Ile	Ala	Phe	Ala	Lys	Ala	
						275				280				285		
atc	aat	gac	ccc	gta	ggc	cac	tat	tcc	aaa	ccc	gag	gcc	acc	cgt	ctg	912
Ile	Asn	Asp	Pro	Val	Gly	His	Tyr	Ser	Lys	Pro	Glu	Ala	Thr	Arg	Leu	
						290				295				300		
gtg	ctg	gac	ttg	ggg	cac	cga	gac	ccc	atg	act	cg	gtg	cac	tcc	aaa	960
Val	Leu	Asp	Leu	Gly	His	Arg	Asp	Pro	Met	Thr	Arg	Val	His	Ser	Lys	
						305				310				315		320
agc	gtg	acc	agg	gaa	gag	gct	ccc	gag	caa	ggt	gtg	caa	agc	aag	att	1008
Ser	Val	Thr	Arg	Glu	Glu	Ala	Pro	Glu	Gln	Gly	Val	Gln	Ser	Lys	Ile	
						325				330				335		
gcc	tca	gtc	gct	atc	agc	cat	cca	cag	gac	tcg	gac	aca	ctg	cta	gtg	1056
Ala	Ser	Val	Ala	Ile	Ser	His	Pro	Gln	Asp	Ser	Asp	Thr	Leu	Leu	Val	
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caa	gag	ccg	tct	tga												1071
Gln	Glu	Pro	Ser													
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<212> PRT

<213> Alcaligenes faecalis

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Met Gln Thr Arg Lys Ile Val Arg Ala Ala Val Gln Ala Ala Ser

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Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala

20 25 30

Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr

35 40 45

Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
 50 55 60
 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
 65 70 75 80
 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
 85 90 95
 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
 100 105 110
 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
 115 120 125
 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
 130 135 140
 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
 145 150 155 160
 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
 165 170 175
 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
 180 185 190
 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
 195 200 205
 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
 210 215 220
 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
 225 230 235 240
 Asn Ala Pro Leu Leu Lys Val Gly Gly Ser Ser Met Ile Phe Ala
 245 250 255
 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
 260 265 270
 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
 275 280 285
 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
 290 295 300
 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
 305 310 315 320
 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
 325 330 335
 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
 340 345 350
 Gln Glu Pro Ser
 355